

FIG.1A

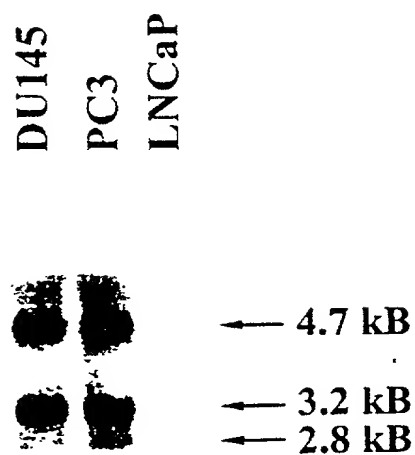


FIG.1B

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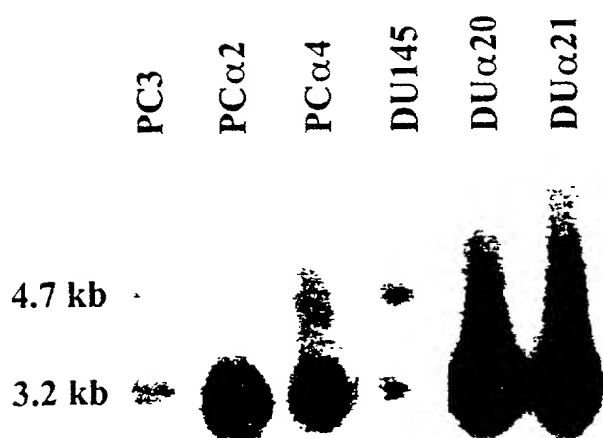
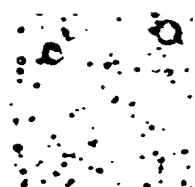


FIG.2



DU145



DUα20



DUα21

FIG.3A



PC3



PCα2



PCα4

FIG.3B

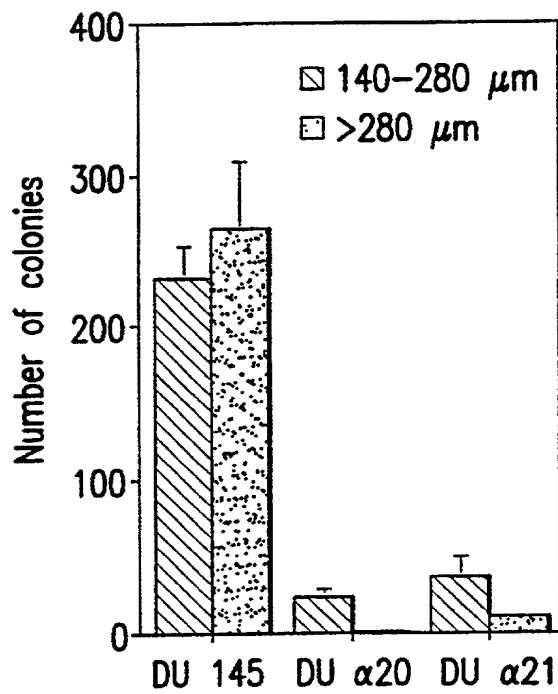


FIG.3A-1

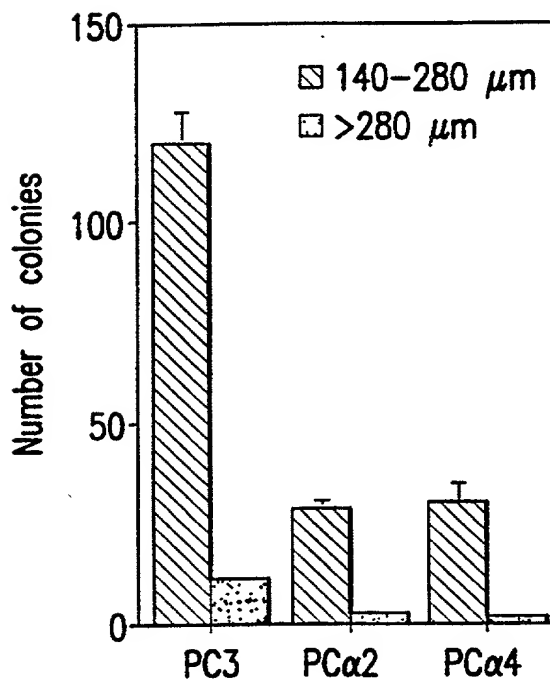


FIG.3B-1

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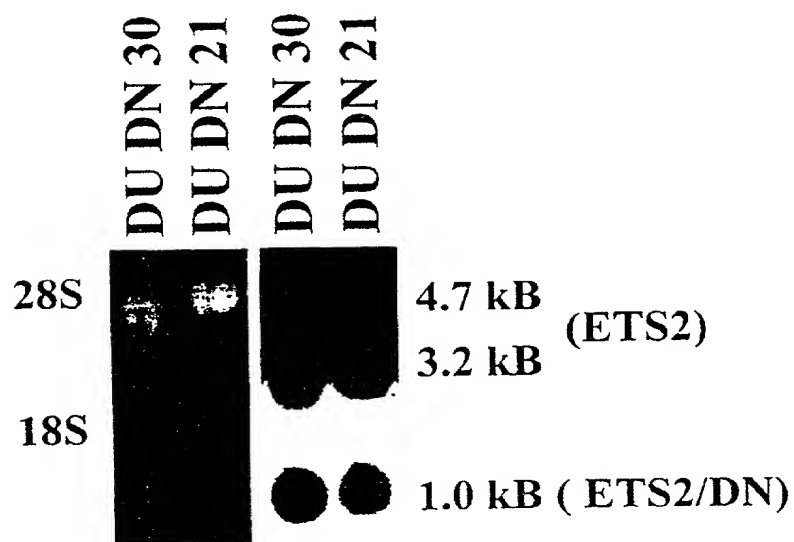


FIG.4A

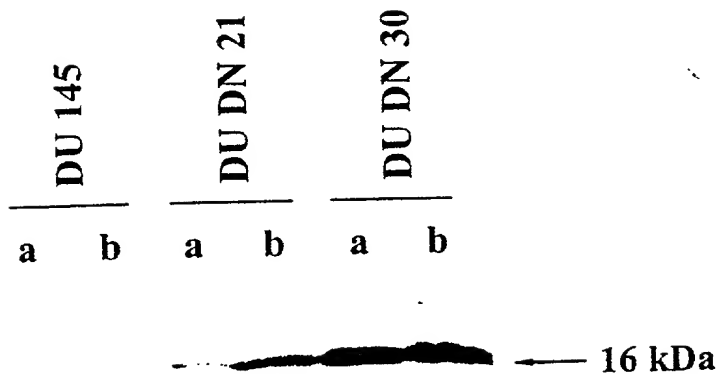


FIG.4B

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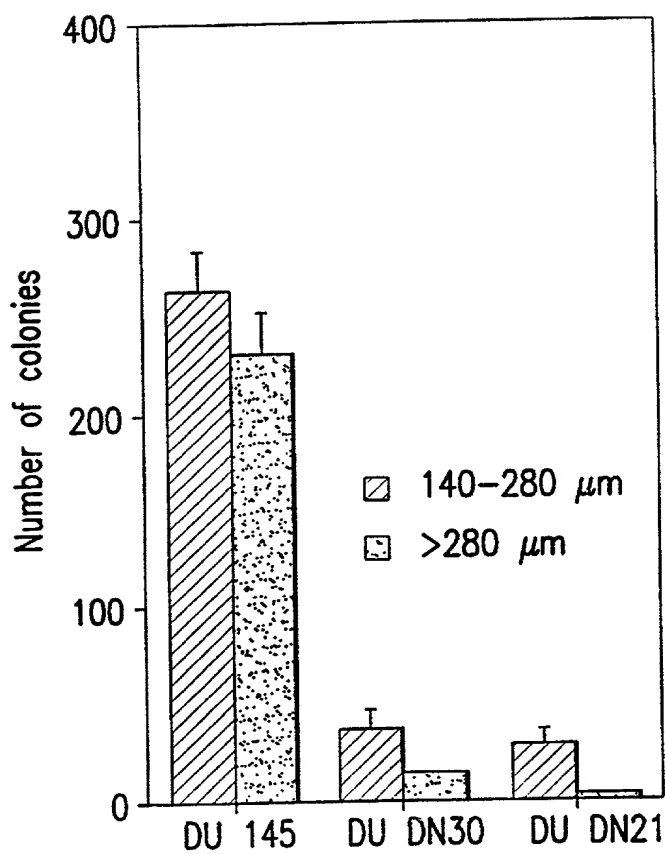


FIG. 5

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CCGTTTCCTC CCCTCCCCTC CACTCGGCCG TCCCTCCTTC CTCCTCCCTC CTCCTCCTC 60
 CTCCTCCCTC TGAAGAGCGC GCGCGGTGGG GGACGGCCCG GTTACTTCCT CCAGAGACTG 120
 ACGAGTGCGG TGTCGCTCCA GCTCAGAGCT CCCGGAGCCG CCCGGCCAGC GTCCGGCCTC 180
 CCTGATCGTC TCTGGCCGGC GCCCTCGCCC TCGCCCGGCG CGCACCGAGC AGCCGCGGGC 240
 GCGGAGCAGC CACCGTCCCG ACCAAGCGCC GGCCTGCCC GCAGCGGCAG GATGAATGAT 300
 TTCGAATCA AGAATATGGA CCAGGTAGCC CCTGTGGCTA ACAGTTACAG AGGGACACTC 360
 AAGCGCCAGC CAGCCTTTGA CACCTTTGAT GGGTCCCTGT TTGCTGTTTT TCCTTCTCTA 420
 AATGAAGAGC AAACACTGCA AGAAGTGCCA ACAGGCTTGG ATTCCATTTC TCATGACTCC 480
 GCCAACTGTG AATTGCCTTT GTTAACCCCG TGCAGCAAGG CTGTGATGAG TCAAGCCTTA 540
 AAAGCTACCT TCAGTGGCTT CAAAAGGAA CAGCGGCGCC TGGGCATTCC AAAGAACCCC 600
 TGGCTGTGGA GTGAGCAACA GGTATGCCAG TGGCTTCTCT GGGCCACCAA TGAGTTCAGT 660
 CTGCTGAACG TGAATCTGCA GAGGTTCGGC ATGAATGGCC AGATGCTGTG TAACCTTGGC 720
 AAGGAACGCT TTCTGGAGCT GGCACCTGAC TTTGTGGGTG ACATTCTCTG GGAACATCTG 780
 GAGCAAATGA TCAAAGAAA CCAAGAAAAG ACAGAAGATC AATATGAAGA AAATTCACAC 840
 CTCACCTCCG TTCCTCATTG GATTAACAGC AATACATTAG GTTTTGGCAC AGAGCAGGCG 900
 CCCTATGGAA TGCAGACACA GAATTACCCC AAAGGCGGCC TCCTGGACAG CATGTGTCCG 960
 GCCTCCACAC CCAGCGTACT CAGCTCTGAG CAGGAGTTTC AGATGTTCCC CAAGTCTCCG 1020
 CTCAGTCCG TCAGCGTCAC CTACTGCTCT GTGAGTCAGG ACTTCCCAGG CAGCAACTTG 1080
 AATTGCTCA CCAACAATTC TGGGACTCCC AAAGACCAGC ACTCCCCTGA GAACGGTGGC 1140
 GACAGCTTCG AGAGCTCAGA CTCCCTCCTC CAGTCTGGA ACAGCCAGTC GTCCTTGCTG 1200
 GATGTGCAAC GGGTTCCTTC CTTGAGAGC TTCGAAGATG ACTGCAGCCA GTCTCTCTGC 1260
 CTCAATAAGC CAACCATGTC TTCAAGGAT TACATCCAAG AGAGGAGTGA CCCAGTGGAG 1320
 CAAGGCAAAC CAGTTATACC TGCAGCTGTG CTGCGCGGCT TCACAGGAAG TGGACCTATT 1380
 CAGCTGTGGC AGTTTCTCCT GGAGCTGCTA TCAGACAAAT CCTGCCAGTC ATTATCAGC 1440
 TGGACTGGAG ACGGATGGGA GTTTAAGCTC GCGGACCCCG ATGAGGTGGC CCGCCGGTGG 1500
 GGAAAGAGGA AAAATAAGCC CAAGATGAAC TACGAGAAGC TGAGCCGGGG CTTACGCTAC 1560
 TATTACGACA AGAACATCAT CCACAAGAGC TCGGGAAGC GCTACGTGTA CCGCTTCGTG 1620
 TCGACCTCC AGAACTTGCT GGGGTTACG CCCGAGGAAC TGCACGCCAT CCTGGGCGTC 1680
 CAGCCCGACA CGGAGGACTG AGGTGCGCGG GACCACCCTG AGCCGGCCCC AGGCTCGTGG 1740
 ACTGAGTGGG AAGCCATCC TGACCAGCTG CCTCCGAGGA CCCAGGAAAG GCAGGATTGA 1800
 AAATGTCCAG GAAAGTGGCC AAGAAGCAGT GGCTTATTG CATCCCAAAC CACGCTCTT 1860
 GACCAGGCTG CCTCCCTTGT GGCAGCAACG GCACAGCTAA TTCTACTCAC AGTGCTTTTA 1920
 AGTGAAAATG GTCGAGAAAG AGGCACCGGG AAGCCGTCCT GCGGCTGGC AGTCCGTGGG 1980
 ACGGGATGGT TCTGGCTGTT TGAGATTCTC AAAGGAGCGA GCATGTCGTG GACACACACA 2040
 GACTATTTTT AGATTTTCTT TTGCCTTTTG CAACCAGGAA CAGCAAATGC AAAAATCTT 2100
 TGAGAGGGTA GGAGGGTGGG AAGGAAACAA CCATGTCATT TCAGAAGTTA GTTTGTATAT 2160
 ATTATAATAA TCTTATAATT GTTCTCAGAA TCCCTTAACA GTTGTATTTA ACAGAAATTG 2220
 TATATTGTAA TTTAAATAA TTATATAACT GTATTGAAA TAAGAATTC 2269

FIG.6

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Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala
 1 5 10 15
 Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe
 20 25 30
 Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr
 35 40 45
 Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala
 50 55 60
 Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser
 65 70 75 80
 Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg
 85 90 95
 Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys
 100 105 110
 Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn
 115 120 125
 Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys
 130 135 140
 Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp
 145 150 155 160
 Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp
 165 170 175
 Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn
 180 185 190
 Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln
 195 200 205
 Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala
 210 215 220
 Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro
 225 230 235 240
 Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln
 245 250 255
 Asp Phe Pro Gly Ser Asn Leu Asn Leu Thr Asn Asn Ser Gly Thr
 260 265 270
 Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser
 275 280 285
 Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp
 290 295 300
 Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln
 305 310 315 320
 Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln
 325 330 335

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Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala
 340 345 350
 Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe
 355 360 365
 Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp
 370 375 380
 Thr Gly Asp Gly Trp Glu Phe Lys Lau Ala Asp Pro Asp Glu Val Ala
 385 390 395 400
 Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys
 405 410 415
 Leu Ser Arg Gly Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile His Lys
 420 425 430
 Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn
 435 440 445
 Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln
 450 455 460
 Pro Asp Thr Glu Asp
 465

FIG.7B

FIG. 8A

FIG. 8B

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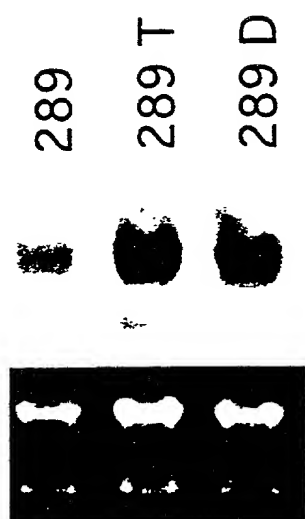


FIG.9A

ETS1 IN 289

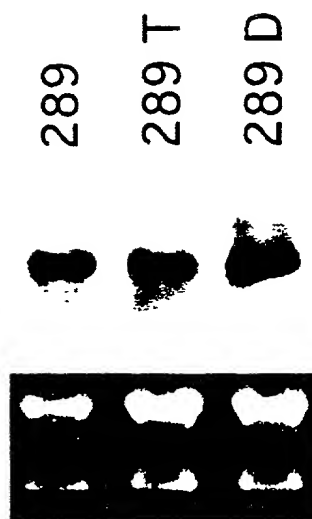


FIG.9B

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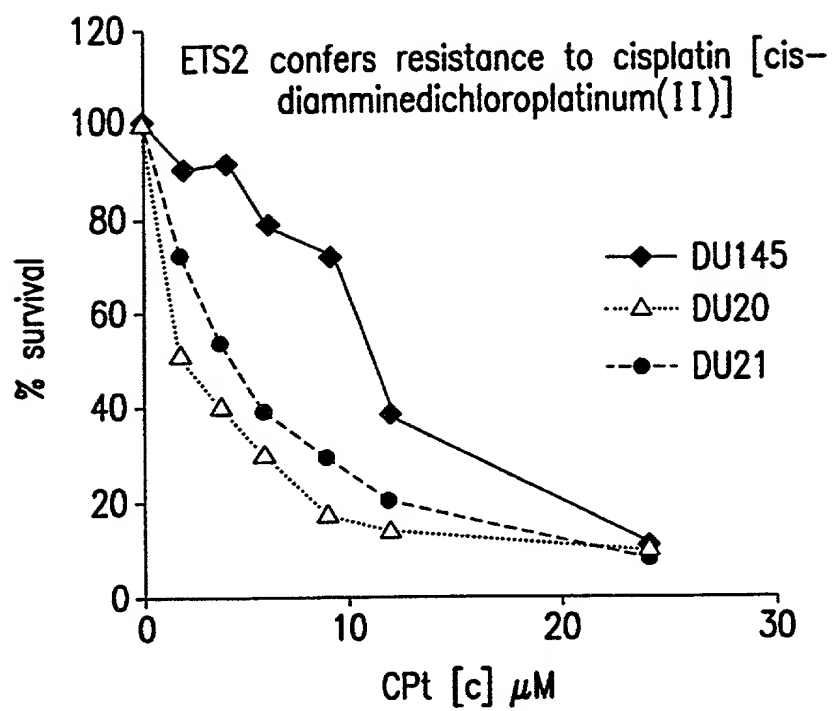


FIG.10